

## SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

WARREN, Patrick V.

SWANSON, Ronald V.

(ii) TITLE OF INVENTION:

TRANSAMINASES AND AMINOTRANSFERASES

(iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Fish and Richardson P.C.
- (B) STREET: 4225 Executive Square, Suite 1400
- (C) CITY: La Jolla
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 92037

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 INCH DISKETTE
- (B) COMPUTER: IBM PS/2
- (C) OPERATING SYSTEM: MS-DOS
- (D) SOFTWARE: WORD PERFECT 5.1

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Unassigned
- (B) FILING DATE: Concurrently
- (C) CLASSIFICATION: Unassigned

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/599,171
- (B) FILING DATE: 2/9/96
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Lisa A. Haile, Ph.D.
- (B) REGISTRATION NUMBER: 38,347
- (C) REFERENCE/DOCKET NUMBER: 09010/016002

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 619-678-5070
- (B) TELEFAX: 619-678-5099

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 52 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGAGAATTC ATAAAGAGG AGAAATTAAC TATGATTGAA GACCCTATGG AC

52

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 31 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAAGATCT TTAAGCACTT CTCTCAGGTT C

31

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 52 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGAATTC ATAAAGAGG AGAAATTAAC TATGGACAGG CTTGAAAAAG TA

52

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 31 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGATCT TCAGCTAACG TTCTCTAACG A

31

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 52 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGACAATTG ATAAAGAGG AGAAATTAAC TATGTGGAA TTAGACCCCTA AA

52

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 31 NUCLEOTIDES
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAGGATCC CTACACCTGT TTTTCAAGCT C

31

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 52 NUCLEOTIDES
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGACAATTG ATAAAGAGG AGAAATTAAC TATGACATAC TTAATGAACA AT

52

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 31 NUCLEOTIDES
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGAAGATCT TTATGAGAAG TCCCTTCAA G

31

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 52 NUCLEOTIDES
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGAGAATTC ATAAAGAGG AGAAATTAAC TATGCGGAAA CTGGCCGAGC GG

52

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 31 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGAGGATCC TTAAAGTGCC GCTTCGATCA A

31

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 52 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGTGCGGG ATAGTCGGAT AC

52

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 31 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGGAAGATCT TTATTCCACC GTGACCGTTT T

31

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 52 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGACAATTG ATTAAAGAGG AGAAATTAAC TATGATAACCC CAGAGGATTA AG

52

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 31 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGGAAGATCT TAAAGAGAG CTTGAAAGGG A

31

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 52 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGAGAACATTCAAAAGAGG AGAAATTAAC TATGAAGCCG TACGCTAAAT AT

52

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 31 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGAAGATCT CTAATACACA GGAGTGATCC A

31

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 1245 NUCLEOTIDES  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG ATT GAA GAC CCT ATG GAC TGG GCT TTT CCG AGG ATA AAG AGA CTG  
Met Ile Glu Asp Pro Met Asp Trp Ala Phe Pro Arg Ile Lys Arg Leu  
5 10 15

48

CCT CAG TAT GTC TTC TCT CTC GTT AAC GAA CTC AAG TAC AAG CTA AGG  
Pro Gln Tyr Val Phe Ser Leu Val Asn Glu Leu Lys Tyr Lys Leu Arg  
20 25 30

96

CGT GAA GGC GAA GAT GTA GTG GAT CTT GGT ATG GGC AAT CCT AAC ATG  
Arg Glu Gly Glu Asp Val Val Asp Leu Gly Met Gly Asn Pro Asn Met  
35 40 45

144

CCT CCA GCA AAG CAC ATA ATA GAT AAA CTC TGC GAA GTG GCT CAA AAG  
Pro Pro Ala Lys His Ile Ile Asp Lys Leu Cys Glu Val Ala Gln Lys  
50 55 60

192

CCG AAC GTT CAC GGA TAT TCT GCG TCA AGG GGC ATA CCA AGA CTG AGA Pro Asn Val His Gly Tyr Ser Ala Ser Arg Gly Ile Pro Arg Leu Arg 65 70 75 80	240
AAG GCT ATA TGT AAC TTC TAC GAA GAA AGG TAC GGA GTG AAA CTC GAC Lys Ala Ile Cys Asn Phe Tyr Glu Glu Arg Tyr Gly Val Lys Leu Asp 85 90 95	288
CCT GAG AGG GAG GCT ATA CTA ACA ATC GGT GCA AAG GAA GGG TAT TCT Pro Glu Arg Glu Ala Ile Leu Thr Ile Gly Ala Lys Glu Gly Tyr Ser 100 105 110	336
CAT TTG ATG CTT GCG ATG ATA TCT CCG GGT GAT ACG GTA ATA GTT CCT His Leu Met Leu Ala Met Ile Ser Pro Gly Asp Thr Val Ile Val Pro 115 120 125	384
AAT CCC ACC TAT CCT ATT CAC TAT TAC GCT CCC ATA ATT GCA GGA GGG Asn Pro Thr Tyr Pro Ile His Tyr Tyr Ala Pro Ile Ile Ala Gly Gly 130 135 140	432
GAA GTT CAC TCA ATA CCC CTT AAC TTC TCG GAC GAT CAA GAT CAT CAG Glu Val His Ser Ile Pro Leu Asn Phe Ser Asp Asp Gln Asp His Gln 145 150 155 160	480
GAA GAG TTT TTA AGG AGG CTT TAC GAG ATA GTA AAA ACC GCG ATG CCA Glu Glu Phe Leu Arg Arg Leu Tyr Glu Ile Val Lys Thr Ala Met Pro 165 170 175	528
AAA CCC AAG GCT GTC GTC ATA AGC TTT CCT CAC AAT CCA ACG ACC ATA Lys Pro Lys Ala Val Val Ile Ser Phe Pro His Asn Pro Thr Thr Ile 180 185 190	576
ACG GTA GAA AAG GAC TTT TTT AAA GAA ATA GTT AAG TTT GCA AAG GAA Thr Val Glu Lys Asp Phe Phe Lys Glu Ile Val Lys Phe Ala Lys Glu 195 200 205	624
CAC GGT CTC TGG ATA ATA CAC GAT TTT GCG TAT GCG GAT ATA GCC TTT His Gly Leu Trp Ile Ile His Asp Phe Ala Tyr Ala Asp Ile Ala Phe 210 215 220	672
GAC GGT TAC AAG CCC CCC TCA ATA CTC GAA ATA GAA GGT GCT AAA GAC Asp Gly Tyr Lys Pro Pro Ser Ile Leu Glu Ile Glu Gly Ala Lys Asp 225 230 235 240	720
GTT GCG GTT GAG CTC TAC TCC ATG TCA AAG GGC TTT TCA ATG GCG GGC Val Ala Val Glu Leu Tyr Ser Met Ser Lys Gly Phe Ser Met Ala Gly 245 250 255	768
TGG AGG GTA GCC TTT GTC GTT GGA AAC GAA ATA CTC ATA AAA AAC CTT Trp Arg Val Ala Phe Val Val Gly Asn Glu Ile Leu Ile Lys Asn Leu 260 265 270	816
GCA CAC CTC AAA AGC TAC TTG GAT TAC GGT ATA TTT ACT CCC ATA CAG Ala His Leu Lys Ser Tyr Leu Asp Tyr Gly Ile Phe Thr Pro Ile Gln 275 280 285	864
GTG GCC TCT ATT ATC GCA TTA GAG AGC CCC TAC GAA ATC GTG GAA AAA Val Ala Ser Ile Ile Ala Leu Glu Ser Pro Tyr Glu Ile Val Glu Lys 290 295 300	912
ACC GCA AAG GTT TAC CAA AAA AGA AGA GAC GTT CTG GTG GAA GGG TTA	960

Thr Ala Lys Val Tyr Gln Lys Arg Arg' Asp Val Leu Val Glu Gly Leu		
305 310 315 320		
AAC AGG CTC GGC TGG AAA GTA AAA CCT AAG GCT ACC ATG TTC GTC		1008
Asn Arg Leu Gly Trp Lys Val Lys Lys Pro Lys Ala Thr Met Phe Val		
325 330 335		
TGG GCA AAG ATT CCC GAA TGG ATA AAT ATG AAC TCT CTG GAC TTT TCC		1056
Trp Ala Lys Ile Pro Glu Trp Ile Asn Met Asn Ser Leu Asp Phe Ser		
340 345 350		
TTG TTC CTC CTA AAA GAG GCG AAG GTT GCG GTA TCC CCG GGT GTG GGC		1104
Leu Phe Leu Leu Lys Glu Ala Lys Val Ala Val Ser Pro Gly Val Gly		
355 360 365		
TTT GGT CAG TAC GGA GAG GGG TAC GTA AGG TTT GCA CTT GTA GAA AAT		1152
Phe Gly Gln Tyr Gly Glu Gly Tyr Val Arg Phe Ala Leu Val Glu Asn		
370 375 380		
GAA CAC AGG ATC AGA CAG GCT ATA AGG GGA ATA AGG AAA GCC TTC AGA		1200
Glu His Arg Ile Arg Gln Ala Ile Arg Gly Ile Arg Lys Ala Phe Arg		
385 390 395 400		
AAA CTC CAG AAG GAG AGG AAA CTT GAA CCT GAG AGA AGT GCT TAA		1245
Lys Leu Gln Lys Glu Arg Lys Leu Glu Pro Glu Arg Ser Ala End		
405 410 414		

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 1122 NUCLEOTIDES  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG GAC AGG CTT GAA AAA GTA TCA CCC TTC ATA GTA ATG GAT ATC CTA		48
Met Asp Arg Leu Glu Lys Val Ser Pro Phe Ile Val Met Asp Ile Leu		
5 10 15		
GCT CAG GCC CAG AAG TAC GAA GAC GTA GTA CAC ATG GAG ATA GGA GAG		96
Ala Gln Ala Gln Lys Tyr Glu Asp Val Val His Met Glu Ile Gly Glu		
20 25 30		
CCC GAT TTA GAA CCG TCT CCC AAG GTA ATG GAA GCT CTG GAA CGT GCG		144
Pro Asp Leu Glu Pro Ser Pro Lys Val Met Glu Ala Leu Glu Arg Ala		
35 40 45		
GTG AAG GAA AAG ACG TTC TAC ACC CCT GCT CTG GGA CTC TGG GAA		192
Val Lys Glu Lys Thr Phe Phe Tyr Thr Pro Ala Leu Gly Leu Trp Glu		
50 55 60		
CTC AGG GAA AGG ATA TCG GAG TTT TAC AGG AAA AAG TAC AGC GTT GAA		240
Leu Arg Glu Arg Ile Ser Glu Phe Tyr Arg Lys Lys Tyr Ser Val Glu		
65 70 75 80		
GTT TCT CCA GAG AGA GTC ATC GTA ACT ACC GGA ACT TCG GGA GCG TTT		288
Val Ser Pro Glu Arg Val Ile Val Thr Thr Gly Thr Ser Gly Ala Phe		
85 90 95		
CTC GTA GCC TAC GCC GTA ACA CTA AAT GCG GGA GAG AAG ATA ATC CTC		336

Leu Val Ala Tyr Ala Val Thr Leu Asn Ala Gly Glu Lys Ile Ile Leu		
100	105	110
CCA GAC CCC TCT TAC CCC TGT TAC AAA AAC TTT GCC TAC CTC TTA GAC		384
Pro Asp Pro Ser Tyr Pro Cys Tyr Lys Asn Phe Ala Tyr Leu Leu Asp		
115	120	125
GCT CAG CCG GTT TTC GTA AAC GTT GAC AAG GAA ACG AAT TAC GAA GTA		432
Ala Gln Pro Val Phe Val Asn Val Asp Lys Glu Thr Asn Tyr Glu Val		
130	135	140
AGG AAA GAG ATG ATA GAA GAC ATT GAT GCG AAA GCC CTT CAC ATT TCC		480
Arg Lys Glu Met Ile Glu Asp Ile Asp Ala Lys Ala Leu His Ile Ser		
145	150	155
TCG CCT CAA AAC CCT ACG GGC ACA CTC TAC TCA CCT GAA ACC CTG AAG		528
Ser Pro Gln Asn Pro Thr Gly Thr Leu Tyr Ser Pro Glu Thr Leu Lys		
165	170	175
GAA CTT GCG GAG TAC TGC GAA GAG AAG GGT ATG TAC TTC ATA TCC GAC		576
Glu Leu Ala Glu Tyr Cys Glu Lys Gly Met Tyr Phe Ile Ser Asp		
180	185	190
GAG ATT TAC CAC GGA CTC GTT TAC GAA GGT AGG GAG CAC ACA GCA CTT		624
Glu Ile Tyr His Gly Leu Val Tyr Glu Gly Arg Glu His Thr Ala Leu		
195	200	205
GAG TTC TCT GAC AGG GCT ATT GTC ATA AAC GGG TTT TCT AAG TAC TTC		672
Glu Phe Ser Asp Arg Ala Ile Val Ile Asn Gly Phe Ser Lys Tyr Phe		
210	215	220
TGT ATG CCA GGT TTC AGG ATA GGG TGG ATG ATA GTT CCG GAA GAA CTC		720
Cys Met Pro Gly Phe Arg Ile Gly Trp Met Ile Val Pro Glu Glu Leu		
225	230	235
240		
GTG AGA AAG GCG GAA ATA GTA ATT CAG AAC GTA TTT ATA TCT GCC CCG		768
Val Arg Lys Ala Glu Ile Val Ile Gln Asn Val Phe Ile Ser Ala Pro		
245	250	255
ACG CTC AGT CAG TAC GCC GCC CTT GAG GCT TTT GAT TAC GAG TAT TTG		816
Thr Leu Ser Gln Tyr Ala Ala Leu Glu Ala Phe Asp Tyr Glu Tyr Leu		
260	265	270
GAG AAG GTA AGA AAA ACC TTT GAA GAG AGG AGG AAC TTC CTT TAT GGG		864
Glu Lys Val Arg Lys Thr Phe Glu Glu Arg Arg Asn Phe Leu Tyr Gly		
275	280	285
GAA CTG AAA AAA CTC TTC AAG ATA GAC GCG AAA CCT CAG GGA GCT TTT		912
Glu Leu Lys Lys Leu Phe Lys Ile Asp Ala Lys Pro Gln Gly Ala Phe		
290	295	300
TAC GTA TGG GCA AAC ATA AGT GAT TAC TCC ACA GAT AGC TAC GAA TTT		960
Tyr Val Trp Ala Asn Ile Ser Asp Tyr Ser Thr Asp Ser Tyr Glu Phe		
305	310	315
320		
GCT TTA AAA CTT TTA AGG GAG GCG AGG GTG GCG GTA ACG CCC GGG GTG		1008
Ala Leu Lys Leu Leu Arg Glu Ala Arg Val Ala Val Thr Pro Gly Val		
325	330	335
GAC TTT GGA AAA AAC AAA ACG AAG GAG TAT ATA AGG TTT GCT TAT ACG		1056
Asp Phe Gly Lys Asn Lys Thr Lys Glu Tyr Ile Arg Phe Ala Tyr Thr		
340	345	350

AGA AAG ATA GAA GAA CTT AAG GAG GGC GTT GAA AGG ATA AAG AAG TTC Arg Lys Ile Glu Glu Leu Lys Glu Gly Val Glu Arg Ile Lys Lys Phe 355 360 365	1104
TTA GAG AAG CTT AGC TGA Leu Glu Lys Leu Ser End 370	1122
(2) INFORMATION FOR SEQ ID NO:19:	
(i) SEQUENCE CHARACTERISTICS	
(A) LENGTH: 1359 NUCLEOTIDES	
(B) TYPE: NUCLEIC ACID	
(C) STRANDEDNESS: SINGLE	
(D) TOPOLOGY: LINEAR	
(ii) MOLECULE TYPE: GENOMIC DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
ATG TGG GAA TTA GAC CCT AAA ACG CTC GAA AAG TGG GAC AAG GAG TAC Met Trp Glu Leu Asp Pro Lys Thr Leu Glu Lys Trp Asp Lys Glu Tyr 5 10 15	48
TTC TGG CAT CCA TTT ACC CAG ATG AAA GTC TAC AGA GAA GAA GAA AAC Phe Trp His Pro Phe Thr Gln Met Lys Val Tyr Arg Glu Glu Asn 20 25 30	96
CTG ATA TTT GAA CGC GGA GAA GGC GTT TAC CTG TGG GAC ATA TAC GGC Leu Ile Phe Glu Arg Gly Glu Gly Val Tyr Leu Trp Asp Ile Tyr Gly 35 40 45	144
AGG AAG TAT ATA GAT GCC ATA TCT TCC CTC TGG TGC AAC GTC CAC GGA Arg Lys Tyr Ile Asp Ala Ile Ser Ser Leu Trp Cys Asn Val His Gly 50 55 60	192
CAT AAC CAC CCT AAA CTG AAC AAC GCA GTT ATG AAA CAG CTC TGT AAG His Asn His Pro Lys Leu Asn Asn Ala Val Met Lys Gln Leu Cys Lys 65 70 75 80	240
GTA GCT CAC ACA ACT ACT CTG GGA AGT TCC AAC GTT CCC GCC ATA CTC Val Ala His Thr Thr Leu Gly Ser Ser Asn Val Pro Ala Ile Leu 85 90 95	288
CTT GCA AAG AAG CTT GTA GAA ATT TCT CCT GAA GGA TTA AAC AAG GTC Leu Ala Lys Lys Leu Val Glu Ile Ser Pro Glu Gly Leu Asn Lys Val 100 105 110	336
TTT TAC TCC GAA GAC GGT GCG GAA GCA GTA GAG ATA GCG ATA AAG ATG Phe Tyr Ser Glu Asp Gly Ala Glu Ala Val Glu Ile Ala Ile Lys Met 115 120 125	384
GCT TAT CAC TAC TGG AAG AAC AAG GGA GTT AAA GGG AAA AAC GTT TTC Ala Tyr His Tyr Trp Lys Asn Lys Gly Val Lys Gly Lys Asn Val Phe 130 135 140	432
ATA ACG CTT TCC GAA GCC TAC CAC GGG GAT ACT GTA GGA GCG GTT AGC Ile Thr Leu Ser Glu Ala Tyr His Gly Asp Thr Val Gly Ala Val Ser 145 150 155 160	480
GTA GGG GGT ATA GAA CTC TTC CAC GGA ACT TAT AAA GAT CTC CTT TTC Val Gly Gly Ile Glu Leu Phe His Gly Thr Tyr Lys Asp Leu Leu Phe 165 170 175	528

AAG ACT ATA AAA CTC CCA TCT CCT TAC CTG TAC TGC AAG GAA AAG TAC Lys Thr Ile Lys Leu Pro Ser Pro Tyr Leu Tyr Cys Lys Glu Lys Tyr 180	185	190	576
GGG GAA CTC CCT GAG TGC ACG GCA GAT TTA TTA AAA CAA CTG GAA Gly Glu Leu Cys Pro Glu Cys Thr Ala Asp Leu Leu Lys Gln Leu Glu 195	200	205	624
GAT ATC CTG AAG TCG CGG GAA GAT ATC GTT GCG GTC ATT ATG GAA GCG Asp Ile Leu Lys Ser Arg Glu Asp Ile Val Ala Val Ile Met Glu Ala 210	215	220	672
GGA ATT CAG GCA GCC GCG GGA ATG CTC CCC TTC CCT CCG GGA TTT TTG Gly Ile Gln Ala Ala Ala Gly Met Leu Pro Phe Pro Pro Gly Phe Leu 225	230	235	720
AAA GGC GTA AGG GAG CTT ACG AAG AAA TAC GAC ACT TTA ATG ATA GTT Lys Gly Val Arg Glu Leu Thr Lys Lys Tyr Asp Thr Leu Met Ile Val 245	250	255	768
GAC GAG GTT GCC ACG GGA TTT GGC AGG ACG GGA ACN ATG TTT TAC TGT Asp Glu Val Ala Thr Gly Phe Gly Arg Thr Gly Thr Met Phe Tyr Cys 260	265	270	816
GAG CAG GAA GGA GTC AGT CCG GAC TTT ATG TGT CTA GGT AAG GGT ATA Glu Gln Glu Gly Val Ser Pro Asp Phe Met Cys Leu Gly Lys Gly Ile 275	280	285	864
ACC GGA GGG TAC CTC CCG CTT GCT GCG ACA CTC ACA ACG GAC GAG GTG Thr Gly Gly Tyr Leu Pro Leu Ala Ala Thr Leu Thr Thr Asp Glu Val 290	295	300	912
TTC AAT GCC TTT TTA GGT GAG TTC GGG GAG GCA AAG CAC TTT TAC CAC Phe Asn Ala Phe Leu Gly Glu Phe Gly Ala Lys His Phe Tyr His 305	310	315	960
GGG CAC ACC TAC ACT GGA AAT AAC CTC GCC TGT TCC GTT GCA CTC GCA Gly His Thr Tyr Thr Gly Asn Asn Leu Ala Cys Ser Val Ala Leu Ala 325	330	335	1008
AAC TTA GAA GTT TTT GAG GAA GAA AGA ACT TTA GAG AAG CTC CAA CCA Asn Leu Glu Val Phe Glu Glu Glu Arg Thr Leu Glu Lys Leu Gln Pro 340	345	350	1056
AAG ATA AAG CTT TTA AAG GAA AGG CTT CAG GAG TTC TGG GAA CTC AAG Lys Ile Lys Leu Leu Lys Glu Arg Leu Gln Glu Phe Trp Glu Leu Lys 355	360	365	1104
CAC GTT GGA GAT GTT AGA CAG CTA GGT TTT ATG GCT GGA ATA GAG CTG His Val Gly Asp Val Arg Gln Leu Gly Phe Met Ala Gly Ile Glu Leu 370	375	380	1152
GTG AAG GAC AAA GAA AAG GGA GAA CCT TTC CCT TAC GGT GAA AGG ACG Val Lys Asp Lys Glu Lys Gly Glu Pro Phe Pro Tyr Gly Glu Arg Thr 385	390	395	1200
GGA TTT AAG GTG GCT TAC AAG TGC AGG GAA AAA GGG GTG TTT TTG AGA Gly Phe Lys Val Ala Tyr Lys Cys Arg Glu Lys Gly Val Phe Leu Arg 405	410	415	1245
CCG CTC GGA GAC GTT ATG GTA TTG ATG ATG CCT CTT GTA ATA GAG GAA Pro Leu Gly Asp Val Met Val Leu Met Met Pro Leu Val Ile Glu Glu			1293

420

425

430

GAC GAA ATG AAC TAC GTT ATT GAT ACA CTT AAA TGG GCA ATT AAA GAG 1341  
 Asp Glu Met Asn Tyr Val Ile Asp Thr Leu Lys Trp Ala Ile Lys Glu  
 435 440 445

CTT GAA AAA GAG GTG TAG 1359  
 Leu Glu Lys Glu Val End  
 450

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1032 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG ACA TAC TTA ATG AAC AAT TAC GCA AGG TTG CCC GTA AAG TTT GTA 48  
 Met Thr Tyr Leu Met Asn Asn Tyr Ala Arg Leu Pro Val Lys Phe Val  
 5 10 15

AGG GGA AAA GGT GTT TAC CTG TAC GAT GAG GAA GGA AAG GAG TAT CTT 96  
 Arg Gly Lys Gly Val Tyr Leu Tyr Asp Glu Glu Gly Lys Glu Tyr Leu  
 20 25 30

GAC TTT GTC TCC GGT ATA GGC GTC AAC TCC CTC GGT CAC GCT TAC CCA 144  
 Asp Phe Val Ser Gly Ile Gly Val Asn Ser Leu Gly His Ala Tyr Pro  
 35 40 45

AAA CTC ACA GAA GCT CTA AAA GAA CAG GTT GAG AAA CTC CTC CAC GTT 192  
 Lys Leu Thr Glu Ala Leu Lys Glu Gln Val Glu Lys Leu Leu His Val  
 50 55 60

TCA AAT CTT TAC GAA AAC CCG TGG CAG GAA GAA CTG GCT CAC AAA CTT 240  
 Ser Asn Leu Tyr Glu Asn Pro Trp Gln Glu Leu Ala His Lys Leu  
 65 70 75 80

GTA AAA CAC TTC TGG ACA GAA GGG AAG GTA TTT TTC GCA AAC AGC GGA 288  
 Val Lys His Phe Trp Thr Glu Gly Lys Val Phe Phe Ala Asn Ser Gly  
 85 90 95

ACG GAA AGT GTA GAG GCG GCT ATA AAG CTC GCA AGG AAG TAC TGG AGG 336  
 Thr Glu Ser Val Glu Ala Ala Ile Lys Leu Ala Arg Lys Tyr Trp Arg  
 100 105 110

GAT AAA GGA AAG AAC AAG TGG AAG TTT ATA TCC TTT GAA AAC TCT TTC 384  
 Asp Lys Gly Lys Asn Lys Trp Lys Phe Ile Ser Phe Glu Asn Ser Phe  
 115 120 125

CAC GGG AGA ACC TAC GGT AGC CTC TCC GCA ACG GGA CAG CCA AAG TTC 432  
 His Gly Arg Thr Tyr Gly Ser Leu Ser Ala Thr Gly Gln Pro Lys Phe  
 130 135 140

CAC AAA GGC TTT GAA CCT CTA GTT CCT GGA TTT TCT TAC GCA AAG CTG 480  
 His Lys Gly Phe Glu Pro Leu Val Pro Gly Phe Ser Tyr Ala Lys Leu  
 145 150 155 160

AAC GAT ATA GAC AGC GTT TAC AAA CTC CTA GAC GAG GAA ACC GCG GGG 528

Asn Asp Ile Asp Ser Val Tyr Lys Leu Leu Asp Glu Glu Thr Ala Gly			
165	170	175	
ATA ATT ATT GAA GTT ATA CAA GGA GAG GGC GGA GTA AAC GAG GCG AGT Ile Ile Ile Glu Val Ile Gln Gly Glu Gly Val Asn Glu Ala Ser		576	
180	185	190	
GAG GAT TTT CTA AGT AAA CTC CAG GAA ATT TGT AAA GAA AAA GAT GTG Glu Asp Phe Leu Ser Lys Leu Gln Glu Ile Cys Lys Glu Lys Asp Val		624	
195	200	205	
CTC TTA ATT ATA GAC GAA GTG CAA ACG GGA ATA GGA AGG ACC GGG GAA Leu Leu Ile Ile Asp Glu Val Gln Thr Gly Ile Gly Arg Thr Gly Glu		672	
210	215	220	
TTC TAC GCA TAT CAA CAC TTC AAT CTA AAA CCG GAC GTA ATT GCG CTT Phe Tyr Ala Tyr Gln His Phe Asn Leu Lys Pro Asp Val Ile Ala Leu		720	
225	230	235	240
GCG AAG GGA CTC GGA GGA GGT GTG CCA ATA GGT GCC ATC CTT GCA AGG Ala Lys Gly Leu Gly Gly Val Pro Ile Gly Ala Ile Leu Ala Arg		768	
245	250	255	
GAA GAA GTG GCC CAG AGC TTT ACT CCC GGC TCC CAC GGC TCT ACC TTC Glu Glu Val Ala Gln Ser Phe Thr Pro Gly Ser His Gly Ser Thr Phe		816	
260	265	270	
GGA GGA AAC CCC TTA GCC TGC AGG GCG GGA ACA GTG GTA GTA GAT GAA Gly Gly Asn Pro Leu Ala Cys Arg Ala Gly Thr Val Val Val Asp Glu		864	
275	280	285	
GTT GAA AAA CTC CTG CCT CAC GTA AGG GAA GTG GGG AAT TAC TTC AAA Val Glu Lys Leu Leu Pro His Val Arg Glu Val Gly Asn Tyr Phe Lys		912	
290	295	300	
GAA AAA CTG AAG GAA CTC GGC AAA GGA AAG GTA AAG GGA AGA GGA TTG Glu Lys Leu Lys Glu Leu Gly Lys Gly Val Lys Gly Arg Gly Leu		960	
305	310	315	320
ATG CTC GGT CTT GAA CTT GAA AGA GAG TGT AAA GAT TAC GTT CTC AAG Met Leu Gly Leu Glu Leu Arg Glu Cys Lys Asp Tyr Val Leu Lys		1008	
325	330	335	
GCT CTT GAA AGG GAC TTC TCA TAA Ala Leu Glu Arg Asp Phe Ser End		1032	
340			

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 1197 NUCLEOTIDES
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATG CGG AAA CTG GCC GAG CGG GCG CAG AAA CTG AGC CCC TCT CCC ACC  
Met Arg Lys Leu Ala Glu Arg Ala Gln Lys Leu Ser Pro Ser Pro Thr

CTC TCG GTG GAC ACC AAG GCC AAG GAG CTT TTG CGG CAG GGG GAA AGG Leu Ser Val Asp Thr Lys Ala Lys Glu Leu Leu Arg Gln Gly Glu Arg 20 25 30	96
GTC ATC AAT TTC GGG GCG GGG GAG CCG GAC TTC GAT ACA CCG GAA CAC Val Ile Asn Phe Gly Ala Gly Glu Pro Asp Phe Asp Thr Pro Glu His 35 40 45	144
ATC AAG GAA GCG GCG AAG CGA GCT TTA GAT CAG GGC TTC ACC AAG TAC Ile Lys Glu Ala Ala Lys Arg Ala Leu Asp Gln Gly Phe Thr Lys Tyr 50 55 60	192
ACG CCG GTG GCT GGG ATC TTA CCT CTT CGG GAG GCC ATA TGC GAG AAG Thr Pro Val Ala Gly Ile Leu Pro Leu Arg Glu Ala Ile Cys Glu Lys 65 70 75 80	240
CTT TAC CGC GAC AAT CAA CTG GAA TAC AGC CCG AAT GAG ATC GTG GTC Leu Tyr Arg Asp Asn Gln Leu Glu Tyr Ser Pro Asn Glu Ile Val Val 85 90 95	288
TCC TGT GGC GCC AAG CAT TCT ATT TTC AAC GCT CTG CAG GTC CTC CTG Ser Cys Gly Ala Lys His Ser Ile Phe Asn Ala Leu Gln Val Leu Leu 100 105 110	336
GAC CCG GGG GAC GAG GTG ATA ATC CCC GTC CCC TAC TGG ACT TCC TAT Asp Pro Gly Asp Glu Val Ile Ile Pro Val Pro Tyr Trp Thr Ser Tyr 115 120 125	384
CCG GAG CAG GTG AAG CTG GCG GGA GGG GTG CCG GTT TTC GTC CCC ACC Pro Glu Gln Val Lys Leu Ala Gly Gly Val Pro Val Phe Val Pro Thr 130 135 140	432
TCT CCC GAG AAC GAC TTC AAG CTC AGG CCG GAA GAT CTA CGT GCG GCT Ser Pro Glu Asn Asp Phe Lys Leu Arg Pro Glu Asp Leu Arg Ala Ala 145 150 155 160	480
GTA ACC CCG CGC ACC CGC CTT TTG ATC CTC AAT TCC CCG GCC AAC CCC Val Thr Pro Arg Thr Arg Leu Leu Ile Leu Asn Ser Pro Ala Asn Pro 165 170 175	528
ACA GGC ACC GTT TAC CGC CGG GAG GAA CTT ATC GGC TTA GCG GAG GTA Thr Gly Thr Val Tyr Arg Arg Glu Glu Leu Ile Gly Leu Ala Glu Val 180 185 190	576
GCC CTG GAG GCC GAC CTA TGG ATC TTG TCG GAC GAG ATC TAC GAA AAG Ala Leu Glu Ala Asp Leu Trp Ile Leu Ser Asp Glu Ile Tyr Glu Lys 195 200 205	624
CTG ATC TAC GAC GGG ATG GAG CAC GTG AGC ATA GCC GCG CTC GAC CCG Leu Ile Tyr Asp Gly Met Glu His Val Ser Ile Ala Ala Leu Asp Pro 210 215 220	672
GAG GTC AAA AAG CGC ACG ATT GTG GTA AAC GGT GTT TCC AAG GCT TAC Glu Val Lys Lys Arg Thr Ile Val Val Asn Gly Val Ser Lys Ala Tyr 225 230 235 240	720
GCC ATG ACC GGT TGG CGC ATA GGT TAT GCT GCC GCT CCC CGG CCG ATA Ala Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Ala Pro Arg Pro Ile 245 250 255	768
GCC CAG GCC ATG ACC AAC CTC CAA AGC CAC AGT ACC TCT AAC CCC ACT Ala Gln Ala Met Thr Asn Leu Gln Ser His Ser Thr Ser Asn Pro Thr	816

260

265

270

TCC GTA GCC CAG GCG GCG CTG GCC GCT CTG AAG GGG CCA CAA GAG Ser Val Ala Gln Ala Ala Leu Ala Leu Lys Gly Pro Gln Glu 275	280	285	864
CCG GTG GAG AAC ATG CGC CGG GCT TTT CAA AAG CGG CGG GAT TTC ATC Pro Val Glu Asn Met Arg Arg Ala Phe Gln Lys Arg Arg Asp Phe Ile 290	295	300	912
TGG CAG TAC CTA AAC TCC TTA CCC GGA GTG CGC TGC CCC AAA CCT TTA Trp Gln Tyr Leu Asn Ser Leu Pro Gly Val Arg Cys Pro Lys Pro Leu 305	310	315	960
GGG GCC TTT TAC GTC TTT CCA GAA GTT GAG CGG GCT TTT GGG CCG CCG Gly Ala Phe Tyr Val Phe Pro Glu Val Glu Arg Ala Phe Gly Pro Pro 325	330	335	1008
TCT AAA AGG ACG GGA AAT ACT ACC GCT AGC GAC CTG GCC CTT TTC CTC Ser Lys Arg Thr Gly Asn Thr Ala Ser Asp Leu Ala Leu Phe Leu 340	345	350	1056
CTG GAA GAG ATA AAA GTG GCC ACC GTG GCT GGG GCT GCC TTT GGG GAC Leu Glu Glu Ile Lys Val Ala Thr Val Ala Gly Ala Ala Phe Gly Asp 355	360	365	1104
GAT CGC TAC CTG CGC TTT TCC TAC GCC CTG CGG CTG GAA GAT ATC GAA Asp Arg Tyr Leu Arg Phe Ser Tyr Ala Leu Arg Leu Glu Asp Ile Glu 370	375	380	1152
GAG GGG ATG CAA CGG TTT AAA GAA TTG ATC GAA GCG GCA CTT TAA Glu Gly Met Gln Arg Phe Lys Glu Leu Ile Glu Ala Ala Leu End 385	390	395	1197

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 1779 NUCLEOTIDES
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG TGC GGG ATA GTC GGA TAC GTA GGG AGG GAT TTA GCC CTT CCT ATA Met Cys Gly Ile Val Gly Tyr Val Gly Arg Asp Leu Ala Leu Pro Ile 5	10	15	48
GTC CTC GGA GCT CTT GAG AGA CTC GAA TAC AGG GGT TAC GAC TCC GCG Val Leu Gly Ala Leu Glu Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala 20	25	30	96
GGA GTT GCC CTT ATA GAA GAC GGG AAA CTC ATA GTT GAA AAG AAG AAG Gly Val Ala Leu Ile Glu Asp Gly Lys Leu Ile Val Glu Lys Lys Lys 35	40	45	144
GGA AAG ATA AGG GAA CTC GTT AAA GCG CTA TGG GGA AAG GAT TAC AAG Gly Lys Ile Arg Glu Leu Val Lys Ala Leu Trp Gly Lys Asp Tyr Lys 50	55	60	192

GCT AAA ACG GGT ATA GGT CAC ACA CGC TGG GCA ACC CAC GGA AAG CCC Ala Lys Thr Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Lys Pro 65 70 75 80	240
ACG GAC GAG AAC GCC CAC CCC CAC ACC GAC GAA AAA GGT GAG TTT GCA Thr Asp Glu Asn Ala His Pro His Thr Asp Glu Lys Gly Glu Phe Ala 85 90 95	288
GTA GTT CAC AAC GGG ATA ATA GAA AAC TAC TTA GAA CTA AAA GAG GAA Val Val His Asn Gly Ile Ile Glu Asn Tyr Leu Glu Leu Lys Glu Glu 100 105 110	336
CTA AAG AAG GAA GGT GTA AAG TTC AGG TCC GAA ACA GAC ACA GAA GTT Leu Lys Lys Glu Gly Val Lys Phe Arg Ser Glu Thr Asp Thr Glu Val 115 120 125	384
ATA GCC CAC CTC ATA GCG AAG AAC TAC AGG GGG GAC TTA CTG GAG GCC Ile Ala His Leu Ile Ala Lys Asn Tyr Arg Gly Asp Leu Leu Glu Ala 130 135 140	432
GTT TTA AAA ACC GTA AAG AAA TTA AAG GGT GCT TTT GCC TTT GCG GTT Val Leu Lys Thr Val Lys Lys Leu Lys Gly Ala Phe Ala Phe Ala Val 145 150 155 160	480
ATA ACG GTT CAC GAA CCA AAC AGA CTA ATA GGA GTG AAG CAG GGG AGT Ile Thr Val His Glu Pro Asn Arg Leu Ile Gly Val Lys Gln Gly Ser 165 170 175	528
CCT TTA ATC GTC GGA CTC GGA GAA GGA AAC TTC CTC GCT TCA GAT Pro Leu Ile Val Gly Leu Gly Glu Asn Phe Leu Ala Ser Asp 180 185 190	576
ATT CCC GCA ATA CTT CCT TAC ACG AAA AAG ATT ATT GTT CTT GAT GAC Ile Pro Ala Ile Leu Pro Tyr Thr Lys Lys Ile Ile Val Leu Asp Asp 195 200 205	624
GGG GAA ATA GCG GAC CTG ACT CCC GAC ACT GTG AAC ATT TAC AAC TTT Gly Glu Ile Ala Asp Leu Thr Pro Asp Thr Val Asn Ile Tyr Asn Phe 210 215 220	672
GAG GGA GAG CCC GTT TCA AAG GAA GTA ATG ATT ACG CCC TGG GAT CTT Glu Gly Glu Pro Val Ser Lys Glu Val Met Ile Thr Pro Trp Asp Leu 225 230 235 240	720
GTT TCT GCG GAA AAG GGT GGT TTT AAA CAC TTC ATG CTA AAA GAG ATA Val Ser Ala Glu Lys Gly Phe Lys His Phe Met Leu Lys Glu Ile 245 250 255	768
TAC GAA CAG CCC AAA GCC ATA AAC GAC ACA CTC AAG GGT TTC CTC TCA Tyr Glu Gln Pro Lys Ala Ile Asn Asp Thr Leu Lys Gly Phe Leu Ser 260 265 270	816
ACC GAA GAC GCA ATA CCC TTT AAG TTA AAA GAC TTC AGA AGG GTT TTA Thr Glu Asp Ala Ile Pro Phe Lys Leu Lys Asp Phe Arg Arg Val Leu 275 280 285	864
ATA ATA GCG TGC GGG ACC TCT TAC CAC GCG GGC TTC GTC GGA AAG TAC Ile Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Phe Val Gly Lys Tyr 290 295 300	912
TGG ATA GAG AGA TTT GCA GGT GTT CCC ACA GAG GTA ATT TAC GCT TCG Trp Ile Glu Arg Phe Ala Gly Val Pro Thr Glu Val Ile Tyr Ala Ser	960

305	310	315	320	
GAA TTC AGG TAT GCG GAC GTT CCC GTT TCG GAC AAG GAT ATC GTT ATC Glu Phe Arg Tyr Ala Asp Val Pro Val Ser Asp Lys Asp Ile Val Ile 325		330	335	1008
GGA ATT TCC CAG TCA GGA GAG ACC GCT GAC ACA AAG TTT GCC CTT CAG Gly Ile Ser Gln Ser Gly Glu Thr Ala Asp Thr Lys Phe Ala Leu Gln 340	345		350	1056
TCC GCA AAG GAA AAG GGA GCC TTT ACC GTG GGA CTC GTA AAC GTA GTG Ser Ala Lys Glu Lys Gly Ala Phe Thr Val Gly Leu Val Asn Val Val 355	360	365		1104
GGA AGT GCC ATA GAC AGG GAG TCG GAC TTT TCC CTT CAC ACA CAT GCG Gly Ser Ala Ile Asp Arg Glu Ser Asp Phe Ser Leu His Thr His Ala 370	375	380		1152
GGA CCC GAA ATA GGC GTG GCG GCT ACA AAG ACC TTC ACC GCA CAG TTC Gly Pro Glu Ile Gly Val Ala Ala Thr Lys Thr Phe Thr Ala Gln Phe 385	390	395	400	1200
ACC GCA CTC TAC GCC CTT TCG GTA AGG GAA AGT GAG GAG AGG GAA AAT Thr Ala Leu Tyr Ala Leu Ser Val Arg Glu Ser Glu Arg Glu Asn 405	410		415	1248
CTA ATA AGA CTC CTT GAA AAG GTT CCA TCA CTC GTT GAA CAA ACA CTG Leu Ile Arg Leu Leu Glu Lys Val Pro Ser Leu Val Glu Gln Thr Leu 420	425	430		1296
AAC ACC GCA GAA GAA GTG GAG AAG GTA GCG GAA AAG TAC ATG AAA AAG Asn Thr Ala Glu Glu Val Glu Lys Val Ala Glu Lys Tyr Met Lys Lys 435	440	445		1344
AAA AAC ATG CTT TAC CTC GGA AGG TAC TTA AAT TAC CCC ATA GCG CTG Lys Asn Met Leu Tyr Leu Gly Arg Tyr Leu Asn Tyr Pro Ile Ala Leu 450	455	460		1392
GAG GGA GCT CTT AAA CTT AAA GAA ATT TCT TAC ATA CAC GCG GAA GGT Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Gly 465	470	475	480	1440
TAT CCC GCA GGG GAG ATG AAG CAC GGT CCC ATA GCC CTC ATA GAC GAA Tyr Pro Ala Gly Glu Met Lys His Gly Pro Ile Ala Leu Ile Asp Glu 485	490	495		1488
AAC ATG CCG GTT GTG GTA ATC GCA CCG AAA GAC AGG GTT TAC GAG AAG Asn Met Pro Val Val Ile Ala Pro Lys Asp Arg Val Tyr Glu Lys 500	505	510		1536
ATA CTC TCA AAC GTA GAA GAG GTT CTC GCA AGA AAG GGA AGG GTT ATT Ile Leu Ser Asn Val Glu Glu Val Leu Ala Arg Lys Gly Arg Val Ile 515	520	525		1584
TCT GTA GGC TTT AAA GGA GAC GAA ACT CTC AAA AGC AAA TCC GAG AGC Ser Val Gly Phe Lys Gly Asp Glu Thr Leu Lys Ser Lys Ser Glu Ser 530	535	540		1632
GTT ATG GAA ATC CCG AAG GCA GAA GAA CCG ATA ACT CCT TTC TTG ACG Val Met Glu Ile Pro Lys Ala Glu Glu Pro Ile Thr Pro Phe Leu Thr 545	550	555	560	1680
GTA ATA CCC CTG CAA CTC TTT GCC TAC TTT ATA GCG AGC AAA CTG GGA Val Ile Pro Leu Gln Leu Phe Ala Tyr Ile Ala Ser Lys Leu Gly				1728

565	570	575	580
CTG GAT GTG GAT CAG CCG AGA AAT CTC GCC AAA ACG GTC ACG GTG GAA Leu Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Thr Val Thr Val Glu 580	585	590	1776
TAA End			1779
<p>(2) INFORMATION FOR SEQ ID NO:23:</p> <p>(i) SEQUENCE CHARACTERISTICS</p> <ul style="list-style-type: none"> <li>(A) LENGTH: 1065 NUCLEOTIDES</li> <li>(B) TYPE: NUCLEIC ACID</li> <li>(C) STRANDEDNESS: SINGLE</li> <li>(D) TOPOLOGY: LINEAR</li> </ul> <p>(ii) MOLECULE TYPE: GENOMIC DNA</p> <p>(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:</p>			
ATG ATA CCC CAG AGG ATT AAG GAA CTT GAA GCT TAC AAG ACG GAG GTC Met Ile Pro Gln Arg Ile Lys Glu Leu Glu Ala Tyr Lys Thr Glu Val 5 10 15			48
ACT CCC GCC TCC GTC AGG CTT TCC TCT AAC GAA TTC CCC TAC GAC TTT Thr Pro Ala Ser Val Arg Leu Ser Ser Asn Glu Phe Pro Tyr Asp Phe 20 25 30			96
CCC GAG GAG ATA AAA CAA AGG GCC TTA GAA GAA TTA AAA AAG GTT CCC Pro Glu Glu Ile Lys Gln Arg Ala Leu Glu Glu Leu Lys Lys Val Pro 35 40 45			144
TTG AAC AAA TAC CCA GAC CCC GAA GCG AAA GAG TTA AAA GCG GTT CTT Leu Asn Lys Tyr Pro Asp Pro Glu Ala Lys Glu Leu Lys Ala Val Leu 50 55 60			192
GCG GAT TTT TTC GGC GTT AAG GAA GAA AAT TTA GTT CTC GGT AAC GGT Ala Asp Phe Phe Gly Val Lys Glu Glu Asn Leu Val Leu Gly Asn Gly 65 70 75 80			240
TCG GAC GAA CTC ATA TAC TAC CTC TCA ATA GCT ATA GGT GAA CTT TAC Ser Asp Glu Leu Ile Tyr Tyr Leu Ser Ile Ala Ile Gly Glu Leu Tyr 85 90 95			288
ATA CCC GTT TAC ATA CCT GTT CCC ACC TTT CCC ATG TAC GAG ATA AGT Ile Pro Val Tyr Ile Pro Val Pro Thr Phe Pro Met Tyr Glu Ile Ser 100 105 110			336
GCG AAA GTT CTC GGA AGA CCC CTC GTA AAG GTT CAA CTG GAC GAA AAC Ala Lys Val Leu Gly Arg Pro Leu Val Lys Val Gln Leu Asp Glu Asn 115 120 125			384
TTT GAT ATA GAC TTA GAA AGA AGT ATT GAA TTA ATA GAG AAA GAA AAA Phe Asp Ile Asp Leu Glu Arg Ser Ile Glu Leu Ile Glu Lys Glu Lys 130 135 140			432
CCC GTT CTC GGG TAC TTT GCT TAC CCA AAC AAC CCC ACG GGA AAC CTC Pro Val Leu Gly Tyr Phe Ala Tyr Pro Asn Asn Pro Thr Gly Asn Leu 145 150 155 160			480
TTT TCC AGG GGA AAG ATT GAG GAG ATA AGA AAC AGG GGT GTT TTC TGT Phe Ser Arg Gly Lys Ile Glu Glu Ile Arg Asn Arg Gly Val Phe Cys			528

165	170	175	
GTA ATA GAC GAA GCC TAC TAT CAT TAC TCC GGA GAA ACC TTT CTG GAA Val Ile Asp Glu Ala Tyr Tyr His Tyr Ser Gly Glu Thr Phe Leu Glu 180	185	190	576
GAC GCG CTC AAA AGG GAA GAT ACG GTA GTT TTG AGG ACA CTT TCA AAA Asp Ala Leu Lys Arg Glu Asp Thr Val Val Leu Arg Thr Leu Ser Lys 195	200	205	624
ATC GGT ATG GCG AGT TTA AGG GTA GGG ATT TTA ATA GGG AAG GGG GAA Ile Gly Met Ala Ser Leu Arg Val Gly Ile Leu Ile Gly Lys Gly Glu 210	215	220	672
ATC GTC TCA GAA ATT AAC AAG GTG AGA CTC CCC TTC AAC GTG ACC TAC Ile Val Ser Glu Ile Asn Lys Val Arg Leu Pro Phe Asn Val Thr Tyr 225	230	235	720
CCC TCT CAG GTG ATG GCA AAA GTT CTC CTC ACG GAG GGA AGA GAA TTC Pro Ser Gln Val Met Ala Lys Val Leu Leu Thr Glu Gly Arg Glu Phe 245	250	255	768
CTA ATG GAA AAG ATA CAG GAG GTT GTA ACA GAG CGA GAA AGG ATG TAC Leu Met Glu Lys Ile Gln Glu Val Val Thr Glu Arg Glu Arg Met Tyr 260	265	270	816
GAC GAA ATG AAG AAA ATA GAA GGA GTT GAG GTT TTT CCG AGT AAG GCT Asp Glu Met Lys Lys Ile Glu Gly Val Glu Val Phe Pro Ser Lys Ala 275	280	285	864
AAC TTC TTG CTT TTC AGA ACG CCT TAC CCC GCC CAC GAG GTT TAT CAG Asn Phe Leu Leu Phe Arg Thr Pro Tyr Pro Ala His Glu Val Tyr Gln 290	295	300	912
GAG CTA CTG AAA AGG GAT GTC CTC AGC AAC GTA TCT TAC ATG GAA Glu Leu Leu Lys Arg Asp Val Leu Val Arg Asn Val Ser Tyr Met Glu 305	310	315	960
GGA CTC CAA AAG TGC CTC AGG GTA AGC GTA GGG AAA CCG GAA GAA AAC Gly Leu Gln Lys Cys Leu Arg Val Ser Val Gly Lys Pro Glu Glu Asn 325	330	335	1008
AAC AAG TTT CTG GAA GCA CTG GAG GAG AGT ATA AAA TCC CTT TCA AGC Asn Lys Phe Leu Glu Ala Leu Glu Glu Ser Ile Lys Ser Leu Ser Ser 340	345	350	1056
TCT CTT TAA Ser Leu End			1065

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 912 NUCLEOTIDES
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG AAG CCG TAC GCT AAA TAT ATC TGG CTT GAC GGC AGA ATA CTT AAG

48

Met Lys Pro Tyr Ala Lys Tyr Ile Trp Leu Asp Gly Arg Ile Leu Lys	5 10 15	
TGG GAA GAC GCG AAA ATA CAC GTG TTG ACT CAC GCG CTT CAC TAC GGA Trp Glu Asp Ala Lys Ile His Val Leu Thr His Ala Leu His Tyr Gly	20 25 30	96
ACC TCT ATA TTC GAG GGA ATA AGA GGG TAT TGG AAC GGC GAT AAT TTG Thr Ser Ile Phe Glu Gly Ile Arg Gly Tyr Trp Asn Gly Asp Asn Leu	35 40 45	144
CTC GTC TTT AGG TTA GAA GAA CAC ATC GAC CGC ATG TAC AGA TCG GCT Leu Val Phe Arg Leu Glu His Ile Asp Arg Met Tyr Arg Ser Ala	50 55 60	192
AAG ATA CTA GGC ATA AAT ATT CCG TAT ACA AGA GAG GAA GTC CGC CAA Lys Ile Leu Gly Ile Asn Ile Pro Tyr Thr Arg Glu Glu Val Arg Gln	65 70 75 80	240
GCT GTA CTA GAG ACC ATA AAG GCT AAT AAC TTC CGA GAG GAT GTC TAC Ala Val Leu Glu Thr Ile Lys Ala Asn Asn Phe Arg Glu Asp Val Tyr	85 90 95	288
ATA AGA CCT GTG GCG TTT GTC GCC TCG CAG ACG GTG ACG CTT GAC ATA Ile Arg Pro Val Ala Phe Val Ala Ser Gln Thr Val Thr Leu Asp Ile	100 105 110	336
AGA AAT TTG GAA GTC TCC CTC GCG GTT ATT GTA TTC CCA TTT GGC AAA Arg Asn Leu Glu Val Ser Leu Ala Val Ile Val Phe Pro Phe Gly Lys	115 120 125	384
TAC CTC TCG CCC AAC GGC ATT AAG GCA ACG ATT GTA AGC TGG CGT AGA Tyr Leu Ser Pro Asn Gly Ile Lys Ala Thr Ile Val Ser Trp Arg Arg	130 135 140	432
GTA CAT AAT ACA ATG CTC CCT GTG ATG GCA AAA ATC GGC GGT ATA TAT Val His Asn Thr Met Leu Pro Val Met Ala Lys Ile Gly Gly Ile Tyr	145 150 155 160	480
GTA AAC TCT GTA CTT GCG CTT GTA GAG GCT AGA AGC AGG GGA TTT GAC Val Asn Ser Val Leu Ala Leu Val Glu Ala Arg Ser Arg Gly Phe Asp	165 170 175	528
GAG GCT TTA TTA ATG GAC GTT AAC GGT TAT GTT GTT GAG GGT TCT GGA Glu Ala Leu Leu Met Asp Val Asn Gly Tyr Val Val Glu Gly Ser Gly	180 185 190	576
GAG AAT ATT TTC ATT GTC AGA GGT GGA AGG CTT TTC ACG CCG CCA GTA Glu Asn Ile Phe Ile Val Arg Gly Arg Leu Phe Thr Pro Pro Val	195 200 205	624
CAC GAA TCT ATC CTC GAG GGA ATT ACG AGG GAT ACG GTA ATA AAG CTC His Glu Ser Ile Leu Glu Gly Ile Thr Arg Asp Thr Val Ile Lys Leu	210 215 220	672
AGC GGG GAT GTG GGA CTT CGG GTG GAG GAA AAG CCT ATT ACG AGG GAG Ser Gly Asp Val Gly Leu Arg Val Glu Glu Lys Pro Ile Thr Arg Glu	225 230 235 240	720
GAG GTG TAT ACA GCC GAC GAG GTG TTT TTA GTA GGA ACC GCC GCA GAG Glu Val Tyr Thr Ala Asp Glu Val Phe Leu Val Gly Thr Ala Ala Glu	245 250 255	768

ATA ACG CCA GTG GTG GAG GTT GAC GGC AGA ACA ATC GGC ACA GGC AAG	816
Ile Thr Pro Val Val Glu Val Asp Gly Arg Thr Ile Gly Thr Gly Lys	
260 265 270	
CCG GGC CCC ATT ACG ACA AAA ATA GCT GAG CTG TAC TCA AAC GTC GTG	864
Pro Gly Pro Ile Thr Thr Lys Ile Ala Glu Leu Tyr Ser Asn Val Val	
275 280 285	
AGA GGC AAA GTA GAG AAA TAC TTA AAT TGG ATC ACT CCT GTG TAT TAG	912
Arg Gly Lys Val Glu Lys Tyr Leu Asn Trp Ile Thr Pro Val Tyr End	
290 295 300	

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 414 AMINO ACIDS  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ile Glu Asp Pro Met Asp Trp Ala Phe Pro Arg Ile Lys Arg Leu	
5 10 15	
Pro Gln Tyr Val Phe Ser Leu Val Asn Glu Leu Lys Tyr Lys Leu Arg	
20 25 30	
Arg Glu Gly Glu Asp Val Val Asp Leu Gly Met Gly Asn Pro Asn Met	
35 40 45	
Pro Pro Ala Lys His Ile Ile Asp Lys Leu Cys Glu Val Ala Gln Lys	
50 55 60	
Pro Asn Val His Gly Tyr Ser Ala Ser Arg Gly Ile Pro Arg Leu Arg	
65 70 75 80	
Lys Ala Ile Cys Asn Phe Tyr Glu Glu Arg Tyr Gly Val Lys Leu Asp	
85 90 95	
Pro Glu Arg Glu Ala Ile Leu Thr Ile Gly Ala Lys Glu Gly Tyr Ser	
100 105 110	
His Leu Met Leu Ala Met Ile Ser Pro Gly Asp Thr Val Ile Val Pro	
115 120 125	
Asn Pro Thr Tyr Pro Ile His Tyr Tyr Ala Pro Ile Ile Ala Gly Gly	
130 135 140	
Glu Val His Ser Ile Pro Leu Asn Phe Ser Asp Asp Gln Asp His Gln	
145 150 155 160	
Glu Glu Phe Leu Arg Arg Leu Tyr Glu Ile Val Lys Thr Ala Met Pro	
165 170 175	
Lys Pro Lys Ala Val Val Ile Ser Phe Pro His Asn Pro Thr Thr Ile	
180 185 190	
Thr Val Glu Lys Asp Phe Phe Lys Glu Ile Val Lys Phe Ala Lys Glu	
195 200 205	

His Gly Leu Trp Ile Ile His Asp Phe Ala Tyr Ala Asp Ile Ala Phe  
 210 215 220  
 Asp Gly Tyr Lys Pro Pro Ser Ile Leu Glu Ile Glu Gly Ala Lys Asp  
 225 230 235 240  
 Val Ala Val Glu Leu Tyr Ser Met Ser Lys Gly Phe Ser Met Ala Gly  
 245 250 255  
 Trp Arg Val Ala Phe Val Val Gly Asn Glu Ile Leu Ile Lys Asn Leu  
 260 265 270  
 Ala His Leu Lys Ser Tyr Leu Asp Tyr Gly Ile Phe Thr Pro Ile Gln  
 275 280 285  
 Val Ala Ser Ile Ile Ala Leu Glu Ser Pro Tyr Glu Ile Val Glu Lys  
 290 295 300  
 Thr Ala Lys Val Tyr Gln Lys Arg Arg Asp Val Leu Val Glu Gly Leu  
 305 310 315 320  
 Asn Arg Leu Gly Trp Lys Val Lys Lys Pro Lys Ala Thr Met Phe Val  
 325 330 335  
 Trp Ala Lys Ile Pro Glu Trp Ile Asn Met Asn Ser Leu Asp Phe Ser  
 340 345 350  
 Leu Phe Leu Leu Lys Glu Ala Lys Val Ala Val Ser Pro Gly Val Gly  
 355 360 365  
 Phe Gly Gln Tyr Gly Glu Gly Tyr Val Arg Phe Ala Leu Val Glu Asn  
 370 375 380  
 Glu His Arg Ile Arg Gln Ala Ile Arg Gly Ile Arg Lys Ala Phe Arg  
 385 390 395 400  
 Lys Leu Gln Lys Glu Arg Lys Leu Glu Pro Glu Arg Ser Ala End  
 405 410 414

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 373 AMINO ACIDS  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Asp Arg Leu Glu Lys Val Ser Pro Phe Ile Val Met Asp Ile Leu  
 5 10 15

Ala Gln Ala Gln Lys Tyr Glu Asp Val Val His Met Glu Ile Gly Glu  
 20 25 30

Pro Asp Leu Glu Pro Ser Pro Lys Val Met Glu Ala Leu Glu Arg Ala  
 35 40 45

Val Lys Glu Lys Thr Phe Phe Tyr Thr Pro Ala Leu Gly Leu Trp Glu  
 50 55 60

Leu Arg Glu Arg Ile Ser Glu Phe Tyr Arg Lys Lys Tyr Ser Val Glu

65	70	75	80
Val Ser Pro Glu Arg Val Ile Val Thr Thr Gly Thr Ser Gly Ala Phe			
85	90	95	
Leu Val Ala Tyr Ala Val Thr Leu Asn Ala Gly Glu Lys Ile Ile Leu			
100	105	110	
Pro Asp Pro Ser Tyr Pro Cys Tyr Lys Asn Phe Ala Tyr Leu Leu Asp			
115	120	125	
Ala Gln Pro Val Phe Val Asn Val Asp Lys Glu Thr Asn Tyr Glu Val			
130	135	140	
Arg Lys Glu Met Ile Glu Asp Ile Asp Ala Lys Ala Leu His Ile Ser			
145	150	155	160
Ser Pro Gln Asn Pro Thr Gly Thr Leu Tyr Ser Pro Glu Thr Leu Lys			
165	170	175	
Glu Leu Ala Glu Tyr Cys Glu Glu Lys Gly Met Tyr Phe Ile Ser Asp			
180	185	190	
Glu Ile Tyr His Gly Leu Val Tyr Glu Gly Arg Glu His Thr Ala Leu			
195	200	205	
Glu Phe Ser Asp Arg Ala Ile Val Ile Asn Gly Phe Ser Lys Tyr Phe			
210	215	220	
Cys Met Pro Gly Phe Arg Ile Gly Trp Met Ile Val Pro Glu Glu Leu			
225	230	235	240
Val Arg Lys Ala Glu Ile Val Ile Gln Asn Val Phe Ile Ser Ala Pro			
245	250	255	
Thr Leu Ser Gln Tyr Ala Ala Leu Glu Ala Phe Asp Tyr Glu Tyr Leu			
260	265	270	
Glu Lys Val Arg Lys Thr Phe Glu Glu Arg Arg Asn Phe Leu Tyr Gly			
275	280	285	
Glu Leu Lys Lys Leu Phe Lys Ile Asp Ala Lys Pro Gln Gly Ala Phe			
290	295	300	
Tyr Val Trp Ala Asn Ile Ser Asp Tyr Ser Thr Asp Ser Tyr Glu Phe			
305	310	315	320
Ala Leu Lys Leu Leu Arg Glu Ala Arg Val Ala Val Thr Pro Gly Val			
325	330	335	
Asp Phe Gly Lys Asn Lys Thr Lys Glu Tyr Ile Arg Phe Ala Tyr Thr			
340	345	350	
Arg Lys Ile Glu Glu Leu Lys Glu Gly Val Glu Arg Ile Lys Lys Phe			
355	360	365	
Leu Glu Lys Leu Ser			
370			

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 453 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Trp Glu Leu Asp Pro Lys Thr Leu Glu Lys Trp Asp Lys Glu Tyr  
5 10 15

Phe Trp His Pro Phe Thr Gln Met Lys Val Tyr Arg Glu Glu Asn  
20 25 30

Leu Ile Phe Glu Arg Gly Glu Gly Val Tyr Leu Trp Asp Ile Tyr Gly  
35 40 45

Arg Lys Tyr Ile Asp Ala Ile Ser Ser Leu Trp Cys Asn Val His Gly  
50 55 60

His Asn His Pro Lys Leu Asn Asn Ala Val Met Lys Gln Leu Cys Lys  
65 70 75 80

Val Ala His Thr Thr Leu Gly Ser Ser Asn Val Pro Ala Ile Leu  
85 90 95

Leu Ala Lys Lys Leu Val Glu Ile Ser Pro Glu Gly Leu Asn Lys Val  
100 105 110

Phe Tyr Ser Glu Asp Gly Ala Glu Ala Val Glu Ile Ala Ile Lys Met  
115 120 125

Ala Tyr His Tyr Trp Lys Asn Lys Gly Val Lys Gly Lys Asn Val Phe  
130 135 140

Ile Thr Leu Ser Glu Ala Tyr His Gly Asp Thr Val Gly Ala Val Ser  
145 150 155 160

Val Gly Gly Ile Glu Leu Phe His Gly Thr Tyr Lys Asp Leu Leu Phe  
165 170 175

Lys Thr Ile Lys Leu Pro Ser Pro Tyr Leu Tyr Cys Lys Glu Lys Tyr  
180 185 190

Gly Glu Leu Cys Pro Glu Cys Thr Ala Asp Leu Leu Lys Gln Leu Glu  
195 200 205

Asp Ile Leu Lys Ser Arg Glu Asp Ile Val Ala Val Ile Met Glu Ala  
210 215 220

Gly Ile Gln Ala Ala Ala Gly Met Leu Pro Phe Pro Pro Gly Phe Leu  
225 230 235 240

Lys Gly Val Arg Glu Leu Thr Lys Lys Tyr Asp Thr Leu Met Ile Val  
245 250 255

Asp Glu Val Ala Thr Gly Phe Gly Arg Thr Gly Thr Met Phe Tyr Cys  
260 265 270

Glu Gln Glu Gly Val Ser Pro Asp Phe Met Cys Leu Gly Lys Gly Ile  
 275 280 285  
 Thr Gly Gly Tyr Leu Pro Leu Ala Ala Thr Leu Thr Thr Asp Glu Val  
 290 295 300  
 Phe Asn Ala Phe Leu Gly Glu Phe Gly Glu Ala Lys His Phe Tyr His  
 305 310 315 320  
 Gly His Thr Tyr Thr Gly Asn Asn Leu Ala Cys Ser Val Ala Leu Ala  
 325 330 335  
 Asn Leu Glu Val Phe Glu Glu Glu Arg Thr Leu Glu Lys Leu Gln Pro  
 340 345 350  
 Lys Ile Lys Leu Leu Lys Glu Arg Leu Gln Glu Phe Trp Glu Leu Lys  
 355 360 365  
 His Val Gly Asp Val Arg Gln Leu Gly Phe Met Ala Gly Ile Glu Leu  
 370 375 380  
 Val Lys Asp Lys Glu Lys Gly Glu Pro Phe Pro Tyr Gly Glu Arg Thr  
 385 390 395 400  
 Gly Phe Lys Val Ala Tyr Lys Cys Arg Glu Lys Gly Val Phe Leu Arg  
 405 410 415  
 Pro Leu Gly Asp Val Met Val Leu Met Met Pro Leu Val Ile Glu Glu  
 420 425 430  
 Asp Glu Met Asn Tyr Val Ile Asp Thr Leu Lys Trp Ala Ile Lys Glu  
 435 440 445  
 Leu Glu Lys Glu Val  
 450

- (2) INFORMATION FOR SEQ ID NO:28:
- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 343 AMINO ACIDS
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Thr Tyr Leu Met Asn Asn Tyr Ala Arg Leu Pro Val Lys Phe Val  
 5 10 15  
 Arg Gly Lys Gly Val Tyr Leu Tyr Asp Glu Glu Gly Lys Glu Tyr Leu  
 20 25 30  
 Asp Phe Val Ser Gly Ile Gly Val Asn Ser Leu Gly His Ala Tyr Pro  
 35 40 45  
 Lys Leu Thr Glu Ala Leu Lys Glu Gln Val Glu Lys Leu Leu His Val  
 50 55 60  
 Ser Asn Leu Tyr Glu Asn Pro Trp Gln Glu Glu Leu Ala His Lys Leu  
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 398 AMINO ACIDS  
(B) TYPE: AMINO ACID  
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Arg Lys Leu Ala Glu Arg Ala Gln Lys Leu Ser Pro Ser Pro Thr  
5 10 15

Leu Ser Val Asp Thr Lys Ala Lys Glu Leu Leu Arg Gln Gly Glu Arg  
20 25 30

Val Ile Asn Phe Gly Ala Gly Glu Pro Asp Phe Asp Thr Pro Glu His  
35 40 45

Ile Lys Glu Ala Ala Lys Arg Ala Leu Asp Gln Gly Phe Thr Lys Tyr  
50 55 60

Thr Pro Val Ala Gly Ile Leu Pro Leu Arg Glu Ala Ile Cys Glu Lys  
65 70 75 80

Leu Tyr Arg Asp Asn Gln Leu Glu Tyr Ser Pro Asn Glu Ile Val Val  
85 90 95

Ser Cys Gly Ala Lys His Ser Ile Phe Asn Ala Leu Gln Val Leu Leu  
100 105 110

Asp Pro Gly Asp Glu Val Ile Ile Pro Val Pro Tyr Trp Thr Ser Tyr  
115 120 125

Pro Glu Gln Val Lys Leu Ala Gly Gly Val Pro Val Phe Val Pro Thr  
130 135 140

Ser Pro Glu Asn Asp Phe Lys Leu Arg Pro Glu Asp Leu Arg Ala Ala  
145 150 155 160

Val Thr Pro Arg Thr Arg Leu Leu Ile Leu Asn Ser Pro Ala Asn Pro  
165 170 175

Thr Gly Thr Val Tyr Arg Arg Glu Glu Leu Ile Gly Leu Ala Glu Val  
180 185 190

Ala Leu Glu Ala Asp Leu Trp Ile Leu Ser Asp Glu Ile Tyr Glu Lys  
195 200 205

Leu Ile Tyr Asp Gly Met Glu His Val Ser Ile Ala Ala Leu Asp Pro  
210 215 220

Glu Val Lys Lys Arg Thr Ile Val Val Asn Gly Val Ser Lys Ala Tyr  
225 230 235 240

Ala Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Ala Pro Arg Pro Ile  
245 250 255

Ala Gln Ala Met Thr Asn Leu Gln Ser His Ser Thr Ser Asn Pro Thr  
260 265 270

Ser Val Ala Gln Ala Ala Ala Leu Ala Ala Leu Lys Gly Pro Gln Glu  
275 280 285

Pro Val Glu Asn Met Arg Arg Ala Phe Gln Lys Arg Arg Asp Phe Ile  
290 295 300

Trp Gln Tyr Leu Asn Ser Leu Pro Gly Val Arg Cys Pro Lys Pro Leu  
305 310 315 320

Gly Ala Phe Tyr Val Phe Pro Glu Val Glu Arg Ala Phe Gly Pro Pro  
325 330 335

Ser Lys Arg Thr Gly Asn Thr Thr Ala Ser Asp Leu Ala Leu Phe Leu  
340 345 350

Leu Glu Glu Ile Lys Val Ala Thr Val Ala Gly Ala Ala Phe Gly Asp  
355 360 365

Asp Arg Tyr Leu Arg Phe Ser Tyr Ala Leu Arg Leu Glu Asp Ile Glu  
370 375 380

Glu Gly Met Gln Arg Phe Lys Glu Leu Ile Glu Ala Ala Leu  
385 390 395

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 592 AMINO ACIDS  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Cys Gly Ile Val Gly Tyr Val Gly Arg Asp Leu Ala Leu Pro Ile  
5 10 15

Val Leu Gly Ala Leu Glu Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala  
20 25 30

Gly Val Ala Leu Ile Glu Asp Gly Lys Leu Ile Val Glu Lys Lys Lys  
35 40 45

Gly Lys Ile Arg Glu Leu Val Lys Ala Leu Trp Gly Lys Asp Tyr Lys  
50 55 60

Ala Lys Thr Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Lys Pro  
65 70 75 80

Thr Asp Glu Asn Ala His Pro His Thr Asp Glu Lys Gly Glu Phe Ala  
85 90 95

Val Val His Asn Gly Ile Ile Glu Asn Tyr Leu Glu Leu Lys Glu Glu  
100 105 110

Leu Lys Lys Glu Gly Val Lys Phe Arg Ser Glu Thr Asp Thr Glu Val  
115 120 125

Ile Ala His Leu Ile Ala Lys Asn Tyr Arg Gly Asp Leu Leu Glu Ala  
130 135 140

Val Leu Lys Thr Val Lys Lys Leu Lys Gly Ala Phe Ala Phe Ala Val  
145 150 155 160

Ile Thr Val His Glu Pro Asn Arg Leu Ile Gly Val Lys Gln Gly Ser  
165 170 175

Pro Leu Ile Val Gly Leu Gly Glu Gly Glu Asn Phe Leu Ala Ser Asp  
180 185 190

Ile Pro Ala Ile Leu Pro Tyr Thr Lys Lys Ile Ile Val Leu Asp Asp  
195 200 205

Gly Glu Ile Ala Asp Leu Thr Pro Asp Thr Val Asn Ile Tyr Asn Phe  
210 215 220

Glu Gly Glu Pro Val Ser Lys Glu Val Met Ile Thr Pro Trp Asp Leu  
225 230 235 240

Val Ser Ala Glu Lys Gly Gly Phe Lys His Phe Met Leu Lys Glu Ile  
245 250 255

Tyr Glu Gln Pro Lys Ala Ile Asn Asp Thr Leu Lys Gly Phe Leu Ser  
260 265 270

Thr Glu Asp Ala Ile Pro Phe Lys Leu Lys Asp Phe Arg Arg Val Leu  
275 280 285

Ile Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Phe Val Gly Lys Tyr  
290 295 300

Trp Ile Glu Arg Phe Ala Gly Val Pro Thr Glu Val Ile Tyr Ala Ser  
305 310 315 320

Glu Phe Arg Tyr Ala Asp Val Pro Val Ser Asp Lys Asp Ile Val Ile  
325 330 335

Gly Ile Ser Gln Ser Gly Glu Thr Ala Asp Thr Lys Phe Ala Leu Gln  
340 345 350

Ser Ala Lys Glu Lys Gly Ala Phe Thr Val Gly Leu Val Asn Val Val  
355 360 365

Gly Ser Ala Ile Asp Arg Glu Ser Asp Phe Ser Leu His Thr His Ala  
370 375 380

Gly Pro Glu Ile Gly Val Ala Ala Thr Lys Thr Phe Thr Ala Gln Phe  
385 390 395 400

Thr Ala Leu Tyr Ala Leu Ser Val Arg Glu Ser Glu Glu Arg Glu Asn  
405 410 415

Leu Ile Arg Leu Leu Glu Lys Val Pro Ser Leu Val Glu Gln Thr Leu  
420 425 430

Asn Thr Ala Glu Glu Val Glu Lys Val Ala Glu Lys Tyr Met Lys Lys  
435 440 445

Lys Asn Met Leu Tyr Leu Gly Arg Tyr Leu Asn Tyr Pro Ile Ala Leu  
450 455 460

Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Gly  
465 470 475 480

Tyr Pro Ala Gly Glu Met Lys His Gly Pro Ile Ala Leu Ile Asp Glu  
485 490 495

Asn Met Pro Val Val Val Ile Ala Pro Lys Asp Arg Val Tyr Glu Lys  
500 505 510

Ile Leu Ser Asn Val Glu Glu Val Leu Ala Arg Lys Gly Arg Val Ile  
 515 520 525  
 Ser Val Gly Phe Lys Gly Asp Glu Thr Leu Lys Ser Lys Ser Glu Ser  
 530 535 540  
 Val Met Glu Ile Pro Lys Ala Glu Glu Pro Ile Thr Pro Phe Leu Thr  
 545 550 555 560  
 Val Ile Pro Leu Gln Leu Phe Ala Tyr Phe Ile Ala Ser Lys Leu Gly  
 565 570 575  
 Leu Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Thr Val Thr Val Glu  
 580 585 590

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 354 AMINO ACIDS
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Ile Pro Gln Arg Ile Lys Glu Leu Glu Ala Tyr Lys Thr Glu Val  
 5 10 15  
 Thr Pro Ala Ser Val Arg Leu Ser Ser Asn Glu Phe Pro Tyr Asp Phe  
 20 25 30  
 Pro Glu Glu Ile Lys Gln Arg Ala Leu Glu Glu Leu Lys Lys Val Pro  
 35 40 45  
 Leu Asn Lys Tyr Pro Asp Pro Glu Ala Lys Glu Leu Lys Ala Val Leu  
 50 55 60  
 Ala Asp Phe Phe Gly Val Lys Glu Glu Asn Leu Val Leu Gly Asn Gly  
 65 70 75 80  
 Ser Asp Glu Leu Ile Tyr Tyr Leu Ser Ile Ala Ile Gly Glu Leu Tyr  
 85 90 95  
 Ile Pro Val Tyr Ile Pro Val Pro Thr Phe Pro Met Tyr Glu Ile Ser  
 100 105 110  
 Ala Lys Val Leu Gly Arg Pro Leu Val Lys Val Gln Leu Asp Glu Asn  
 115 120 125  
 Phe Asp Ile Asp Leu Glu Arg Ser Ile Glu Leu Ile Glu Lys Glu Lys  
 130 135 140  
 Pro Val Leu Gly Tyr Phe Ala Tyr Pro Asn Asn Pro Thr Gly Asn Leu  
 145 150 155 160  
 Phe Ser Arg Gly Lys Ile Glu Glu Ile Arg Asn Arg Gly Val Phe Cys  
 165 170 175  
 Val Ile Asp Glu Ala Tyr Tyr His Tyr Ser Gly Glu Thr Phe Leu Glu  
 180 185 190

Asp Ala Leu Lys Arg Glu Asp Thr Val Val Leu Arg Thr Leu Ser Lys  
 195 200 205  
 Ile Gly Met Ala Ser Leu Arg Val Gly Ile Leu Ile Gly Lys Gly Glu  
 210 215 220  
 Ile Val Ser Glu Ile Asn Lys Val Arg Leu Pro Phe Asn Val Thr Tyr  
 225 230 235 240  
 Pro Ser Gln Val Met Ala Lys Val Leu Leu Thr Glu Gly Arg Glu Phe  
 245 250 255  
 Leu Met Glu Lys Ile Gln Glu Val Val Thr Glu Arg Glu Arg Met Tyr  
 260 265 270  
 Asp Glu Met Lys Lys Ile Glu Gly Val Glu Val Phe Pro Ser Lys Ala  
 275 280 285  
 Asn Phe Leu Leu Phe Arg Thr Pro Tyr Pro Ala His Glu Val Tyr Gln  
 290 295 300  
 Glu Leu Leu Lys Arg Asp Val Leu Val Arg Asn Val Ser Tyr Met Glu  
 305 310 315 320  
 Gly Leu Gln Lys Cys Leu Arg Val Ser Val Gly Lys Pro Glu Glu Asn  
 325 330 335  
 Asn Lys Phe Leu Glu Ala Leu Glu Ser Ile Lys Ser Leu Ser Ser  
 340 345 350  
 Ser Leu

- (2) INFORMATION FOR SEQ ID NO:32:
- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 303 AMINO ACIDS
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Lys Pro Tyr Ala Lys Tyr Ile Trp Leu Asp Gly Arg Ile Leu Lys  
 5 10 15  
 Trp Glu Asp Ala Lys Ile His Val Leu Thr His Ala Leu His Tyr Gly  
 20 25 30  
 Thr Ser Ile Phe Glu Gly Ile Arg Gly Tyr Trp Asn Gly Asp Asn Leu  
 35 40 45  
 Leu Val Phe Arg Leu Glu Glu His Ile Asp Arg Met Tyr Arg Ser Ala  
 50 55 60  
 Lys Ile Leu Gly Ile Asn Ile Pro Tyr Thr Arg Glu Glu Val Arg Gln  
 65 70 75 80  
 Ala Val Leu Glu Thr Ile Lys Ala Asn Asn Phe Arg Glu Asp Val Tyr  
 85 90 95

Ile Arg Pro Val Ala Phe Val Ala Ser Gln Thr Val Thr Leu Asp Ile  
100 105 110

Arg Asn Leu Glu Val Ser Leu Ala Val Ile Val Phe Pro Phe Gly Lys  
115 120 125

Tyr Leu Ser Pro Asn Gly Ile Lys Ala Thr Ile Val Ser Trp Arg Arg  
130 135 140

Val His Asn Thr Met Leu Pro Val Met Ala Lys Ile Gly Gly Ile Tyr  
145 150 155 160

Val Asn Ser Val Leu Ala Leu Val Glu Ala Arg Ser Arg Gly Phe Asp  
165 170 175

Glu Ala Leu Leu Met Asp Val Asn Gly Tyr Val Val Glu Gly Ser Gly  
180 185 190

Glu Asn Ile Phe Ile Val Arg Gly Gly Arg Leu Phe Thr Pro Pro Val  
195 200 205

His Glu Ser Ile Leu Glu Gly Ile Thr Arg Asp Thr Val Ile Lys Leu  
210 215 220

Ser Gly Asp Val Gly Leu Arg Val Glu Glu Lys Pro Ile Thr Arg Glu  
225 230 235 240

Glu Val Tyr Thr Ala Asp Glu Val Phe Leu Val Gly Thr Ala Ala Glu  
245 250 255

Ile Thr Pro Val Val Glu Val Asp Gly Arg Thr Ile Gly Thr Gly Lys  
260 265 270

Pro Gly Pro Ile Thr Thr Lys Ile Ala Glu Leu Tyr Ser Asn Val Val  
275 280 285

Arg Gly Lys Val Glu Lys Tyr Leu Asn Trp Ile Thr Pro Val Tyr  
290 295 300